IFWO

RAW SEQUENCE LISTING　　　　　　　　　DATE: 10/12/2004
PATENT APPLICATION:　US/10/678,588A　　　TIME: 11:50:53

Input Set : **D:\52578C_cor.ST25.txt**
Output Set: **N:\CRF4\10122004\J678588A.raw**

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 3 <110> APPLICANT: Wu, Jingrui
 5 <120> TITLE OF INVENTION: Water-Deficit-TolerantTransgenic Plants
 7 <130> FILE REFERENCE: 38-21(52578)C
 9 <140> CURRENT APPLICATION NUMBER: US 10/678,588A
10 <141> CURRENT FILING DATE: 2003-10-02
12 <150> PRIOR APPLICATION NUMBER: US 60/415,758
13 <151> PRIOR FILING DATE: 2002-10-02
15 <150> PRIOR APPLICATION NUMBER: US 60/425,157
16 <151> PRIOR FILING DATE: 2002-11-08
18 <150> PRIOR APPLICATION NUMBER: US 60/463,787
19 <151> PRIOR FILING DATE: 2003-04-11
21 <160> NUMBER OF SEQ ID NOS: 10
23 <170> SOFTWARE: PatentIn version 3.2
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2480
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: transcriptional unit comprising promoter, coding sequence for
32       transcription factor of SEQ ID NO:2 and terminator elements
34 <400> SEQUENCE: 1
35 aggatattaa agtatgtatt catcattaat ataatcagtg tattccaata tgtactacga       60
37 tttccaatgt ctttattgtc gccgtatgta atcggcgtca caaaataatc cccggtgact      120
39 ttcttttaat ccaggatgaa ataatatgtt attataattt ttgcgatttg gtccgttata      180
41 ggaattgaag tgtgcttgag ctcggtcgcc accactccca tttcataatt ttacatgtat      240
43 ttgaaaaata aaaatttatg gtattcaatt taaacacgta tacttgtaaa gaatgatatc      300
45 ttgaaagaaa tatagtttaa atatttattg ataaaataac aagtcaggta ttatagtcca      360
47 agcaaaaaca taaatttatt gatgcaagtt taaattcaga aatatttcaa taactgatta      420
49 tatcagctgg tacattgccg tagatgaaag actgagtgcg atattatgtg taatacataa      480
51 attgatgata tagctagaac tagtggatcc cccgggccct gcaggctcga gctagtttga      540
53 gatatccccg ttatggtact ggggttgcat ataacccatt ccttggttgt atgctccctg      600
55 ttggcccatc ccttgtgcag ctgagctact tgctcccaca tgaccaaggg catccttttt      660
57 aattgagcca tcgctagatt ttgcagttaa cttgctatca ccctccatct ctctgtactt      720
59 ctgcaggtac accttgaggg gttcaatgta gtcttcaaac cccagcgtgg ccatggccca      780
61 cagcagatcg tcgccattga tggtcttccg cttctccctc tggcacttgt cactcgcttc      840
63 gctagtgatg aaggagatga actcggagac gcactcctgc acggtctcct tagcgtcctt      900
65 ggcgatcttc ccgttagccg ggatggtctt cccgttagcc gggatggcct tcttcatgat      960
67 gcgactgatg ttggcgatgg gcaggaacct gtcctgctcc ctgacgctgc caccgcctcc     1020
69 gcctcccctg gggctcccgc tctcgtggct cccgccgccg ccgccagggc tcgccggagc     1080
71 ttccgccatg gtctacctac aaaaaagctc cgcacgaggc tgcatttgtc acaaatcatg     1140
73 aaaagaaaaa ctaccgatga acaatgctga gggattcaaa ttctacccac aaaaagaaga     1200
75 aagaaagatc tagcacatct aagcctgacg aagcagcaga aatatataaa aatataaacc     1260
77 atagtgccct tttcccctct tcctgatctt gtttagcatg gcggaaattt taaacccccc     1320
```

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```
 79 atcatctccc ccaacaacgg cggatcgcag atctacatcc gagagcccca ttccccgcga  1380
 81 gatccgggcc ggatccacgc cggcgagagc cccagccgcg agatcccgcc cctccccgcgc 1440
 83 accgatctgg gcgcgcacga agccgcctct cgcccaccca aactaccaag gccaaagatc  1500
 85 gagaccgaga cggaaaaaaa aaacggagaa agaaagagga gaggggcggg gtggttaccg  1560
 87 gcggcggcgg aggggggaggg gggaggagct cgtcgtccgg cagcgagggg ggaggaggtg  1620
 89 gtggtggtgg tggtggtagg gttgggggga tgggaggaga ggggggggta tgtatatagt  1680
 91 ggcgatgggg ggcgtttctt tggaagcgga gggagggccg gcctcgtcgc tggctcgcga  1740
 93 tcctcctcgc gtttccggcc cccacgaccc ggacccacct gctgtttttt ctttttcttt  1800
 95 tttttctttc tttttttttt tttggctgcg agacgtgcgg tgcgtgcgga caactcacgg  1860
 97 tgatagtggg ggggtgtgga gactattgtc cagttggctg gactggggtg ggttgggttg  1920
 99 ggttgggttg ggctgggctt gctatggatc gtggatagca ctttgggctt taggacttta  1980
101 ggggttgttt ttgtaaatgt tttgagtcta agtttatctt ttattttttac tagaaaaaat  2040
103 acccatgcgc tgcaacgggg gaaagctatt ttaatcttat tattgttcat tgtgagaatt  2100
105 cgcctgaata tatattttc tcaaaaatta tgtcaaatta gcatatgggt tttttttaaag 2160
107 atatttctta tacaaatccc tctgtattta caaaagcaaa cgaacttaaa acccgactca  2220
109 aatacagata tgcatttcca aaagcgaata aacttaaaaa ccaattcata caaaaatgac  2280
111 gtatcaaagt accgacaaaa acatcctcaa tttttataat agtagaaaag agtaaatttc  2340
113 actttgggcc acctttttatt accgatattt tactttatac caccttttaa ctgatgtttt  2400
115 cacttttgac caggtaatct tacctttgtt ttattttgga ctatcccgac tctcttctca  2460
117 agcatatgaa tgacctcgag                                              2480
120 <210> SEQ ID NO: 2
121 <211> LENGTH: 185
122 <212> TYPE: PRT
123 <213> ORGANISM: Zea mays
125 <400> SEQUENCE: 2
127 Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Gly Ser His Glu
128 1               5                   10                  15
131 Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
132               20                  25                  30
135 Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
136           35                  40                  45
139 Ile Pro Ala Asn Gly Lys Thr Ile Pro Ala Asn Gly Lys Ile Ala Lys
140       50                  55                  60
143 Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
144 65                  70                  75                  80
147 Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
148               85                  90                  95
151 Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu
152               100                 105                 110
155 Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met
156           115                 120                 125
159 Glu Gly Asp Ser Lys Leu Thr Ala Lys Ser Ser Asp Gly Ser Ile Lys
160       130                 135                 140
163 Lys Asp Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Ala Gln Gly
164 145                 150                 155                 160
167 Met Gly Gln Gln Gly Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro
168               165                 170                 175
171 Gln Tyr His Asn Gly Asp Ile Ser Asn
172           180                 185
```

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Input Set : **D:\52578C_cor.ST25.txt**
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175 <210> SEQ ID NO: 3
176 <211> LENGTH: 178
177 <212> TYPE: PRT
178 <213> ORGANISM: Zea mays
180 <400> SEQUENCE: 3
182 Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Gly Ser His Glu
183 1               5                   10                  15
186 Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
187             20                  25                  30
190 Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
191         35                  40                  45
194 Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln
195     50                  55                  60
198 Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp
199 65                  70                  75                  80
202 Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu
203             85                  90                  95
206 Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys
207             100                 105                 110
210 Val Tyr Leu Gln Lys Tyr Arg Glu Met Glu Gly Asp Ser Lys Leu Thr
211         115                 120                 125
214 Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp Ala Leu Gly His Val
215     130                 135                 140
218 Gly Ala Ser Ser Ser Ala Ala Glu Gly Met Gly Gln Gln Gly Ala Tyr
219 145                 150                 155                 160
222 Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His Asn Gly Asp Ile
223             165                 170                 175
226 Ser Asn
230 <210> SEQ ID NO: 4
231 <211> LENGTH: 537
232 <212> TYPE: DNA
233 <213> ORGANISM: Zea mays
235 <400> SEQUENCE: 4
236 atggcggaag ctccggcgag ccctggcggc ggcggcggga gccacgagag cgggagcccc    60
238 aggggaggcg gaggcggtgg cagcgtcagg gagcaggaca ggttcctgcc catcgccaac   120
240 atcagtcgca tcatgaagaa ggccatcccg gctaacggga agatcgccaa ggacgctaag   180
242 gagaccgtgc aggagtgcgt ctccgagttc atctccttca tcactagcga agcgagtgac   240
244 aagtgccaga gggagaagcg gaagaccatc aatggcgacg atctgctgtg ggccatggcc   300
246 acgctggggt ttgaagacta cattgaaccc ctcaaggtgt acctacagaa gtacagagag   360
248 atggagggtg atagcaagtt aactgctaaa tctagcgatg gctcgattaa aaaggatgct   420
250 cttggtcatg tgggagcaag tagctcagct gcagaaggga tgggccaaca gggagcatac   480
252 aaccaaggaa tgggttatat gcaacctcag taccataacg gggatatctc aaactaa       537
255 <210> SEQ ID NO: 5
256 <211> LENGTH: 522
257 <212> TYPE: DNA
258 <213> ORGANISM: Glycine max
260 <400> SEQUENCE: 5
261 atgtcggatg cgccaccgag cccgactcat gagagtgggg gcgagcagag cccgcgcggt    60
263 tcgtcgtccg cgcgcaggga gcaggaccgg tacctcccga ttgccaacat cagccgcatt   120
```

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```
265 atgaagaagg ctctgcctcc caacggcaag attgcaaagg atgccaaaga caccatgcag    180
267 gaatgcgttt ctgagttcat cagcttcatt accagcgagg cgagtgagaa atgccagaag    240
269 gagaagagaa agacaatcaa tggagacgat ttgctatggg ccatggccac tttaggattt    300
271 gaagactaca tagagccgct taaggtgtac ctggctaggt acagagaggc ggagggtgac    360
273 actaaaggat ctgctagaag tggtgatgga tctgctacac cagatcaagt tggccttgca    420
275 ggtcaaaatt ctcagcttgt tcatcagggt tcgctgaact atattggttt gcaggtgcaa    480
277 ccacaacatc tggttatgcc ttcaatgcaa agccatgaat ag                       522
280 <210> SEQ ID NO: 6
281 <211> LENGTH: 173
282 <212> TYPE: PRT
283 <213> ORGANISM: Glycine max
285 <400> SEQUENCE: 6
287 Met Ser Asp Ala Pro Pro Ser Pro Thr His Glu Ser Gly Gly Glu Gln
288 1               5                   10                  15
291 Ser Pro Arg Gly Ser Ser Ser Gly Ala Arg Glu Gln Asp Arg Tyr Leu
292             20                  25                  30
295 Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro Asn
296         35                  40                  45
299 Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val Ser
300     50                  55                  60
303 Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln Lys
304 65                  70                  75                  80
307 Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala
308             85                  90                  95
311 Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Ala
312             100                 105                 110
315 Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser Gly
316         115                 120                 125
319 Asp Gly Ser Ala Thr Pro Asp Gln Val Gly Leu Ala Gly Gln Asn Ser
320     130                 135                 140
323 Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val Gln
324 145                 150                 155                 160
327 Pro Gln His Leu Val Met Pro Ser Met Gln Ser His Glu
328             165                 170
331 <210> SEQ ID NO: 7
332 <211> LENGTH: 141
333 <212> TYPE: PRT
334 <213> ORGANISM: Arabidopsis thaliana
336 <400> SEQUENCE: 7
338 Met Ala Asp Thr Pro Ser Ser Pro Ala Gly Asp Gly Gly Glu Ser Gly
339 1               5                   10                  15
342 Gly Ser Val Arg Glu Gln Asp Arg Tyr Leu Pro Ile Ala Asn Ile Ser
343             20                  25                  30
346 Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp
347         35                  40                  45
350 Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
351     50                  55                  60
354 Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val
355 65                  70                  75                  80
```

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Input Set : **D:\52578C_cor.ST25.txt**
Output Set: **N:\CRF4\10122004\J678588A.raw**

```
358 Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
359             85              90              95
362 Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
363            100             105             110
366 Gly Asp Asn Lys Gly Ser Gly Lys Ser Gly Asp Gly Ser Asn Arg Asp
367         115             120             125
370 Ala Gly Gly Gly Val Ser Gly Glu Glu Met Pro Ser Trp
371      130             135             140
374 <210> SEQ ID NO: 8
375 <211> LENGTH: 101
376 <212> TYPE: PRT
377 <213> ORGANISM: Artificial sequence
379 <220> FEATURE:
380 <223> OTHER INFORMATION: protein consensus sequence
383 <220> FEATURE:
384 <221> NAME/KEY: MISC_FEATURE
385 <222> LOCATION: (22)..(22)
386 <223> OTHER INFORMATION: Xaa can be Ala or Pro
388 <220> FEATURE:
389 <221> NAME/KEY: MISC_FEATURE
390 <222> LOCATION: (26)..(26)
391 <223> OTHER INFORMATION: Xaa can be Thr or none
393 <220> FEATURE:
394 <221> NAME/KEY: MISC_FEATURE
395 <222> LOCATION: (27)..(27)
396 <223> OTHER INFORMATION: Xaa can be Ile or none
398 <220> FEATURE:
399 <221> NAME/KEY: MISC_FEATURE
400 <222> LOCATION: (28)..(28)
401 <223> OTHER INFORMATION: Xaa can be Pro or none
403 <220> FEATURE:
404 <221> NAME/KEY: MISC_FEATURE
405 <222> LOCATION: (29)..(29)
406 <223> OTHER INFORMATION: Xaa can be Ala or none
408 <220> FEATURE:
409 <221> NAME/KEY: MISC_FEATURE
410 <222> LOCATION: (30)..(30)
411 <223> OTHER INFORMATION: Xaa can be Asn or none
413 <220> FEATURE:
414 <221> NAME/KEY: MISC_FEATURE
415 <222> LOCATION: (31)..(31)
416 <223> OTHER INFORMATION: Xaa can be Gly or none
418 <220> FEATURE:
419 <221> NAME/KEY: MISC_FEATURE
420 <222> LOCATION: (32)..(32)
421 <223> OTHER INFORMATION: Xaa can be Lys or none
423 <220> FEATURE:
424 <221> NAME/KEY: MISC_FEATURE
425 <222> LOCATION: (39)..(39)
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/12/2004
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Input Set : **D:\52578C_cor.ST25.txt**
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 22,26,27,28,29,30,31,32,39,41,58,62,94,95,99
Seq#:9; Xaa Pos. 29
Seq#:10; Xaa Pos. 2,3,4,6

VERIFICATION SUMMARY   DATE: 10/12/2004
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Input Set : **D:\52578C_cor.ST25.txt**
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```
L:464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:16
L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:32
L:472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:80
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:16
L:541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
```